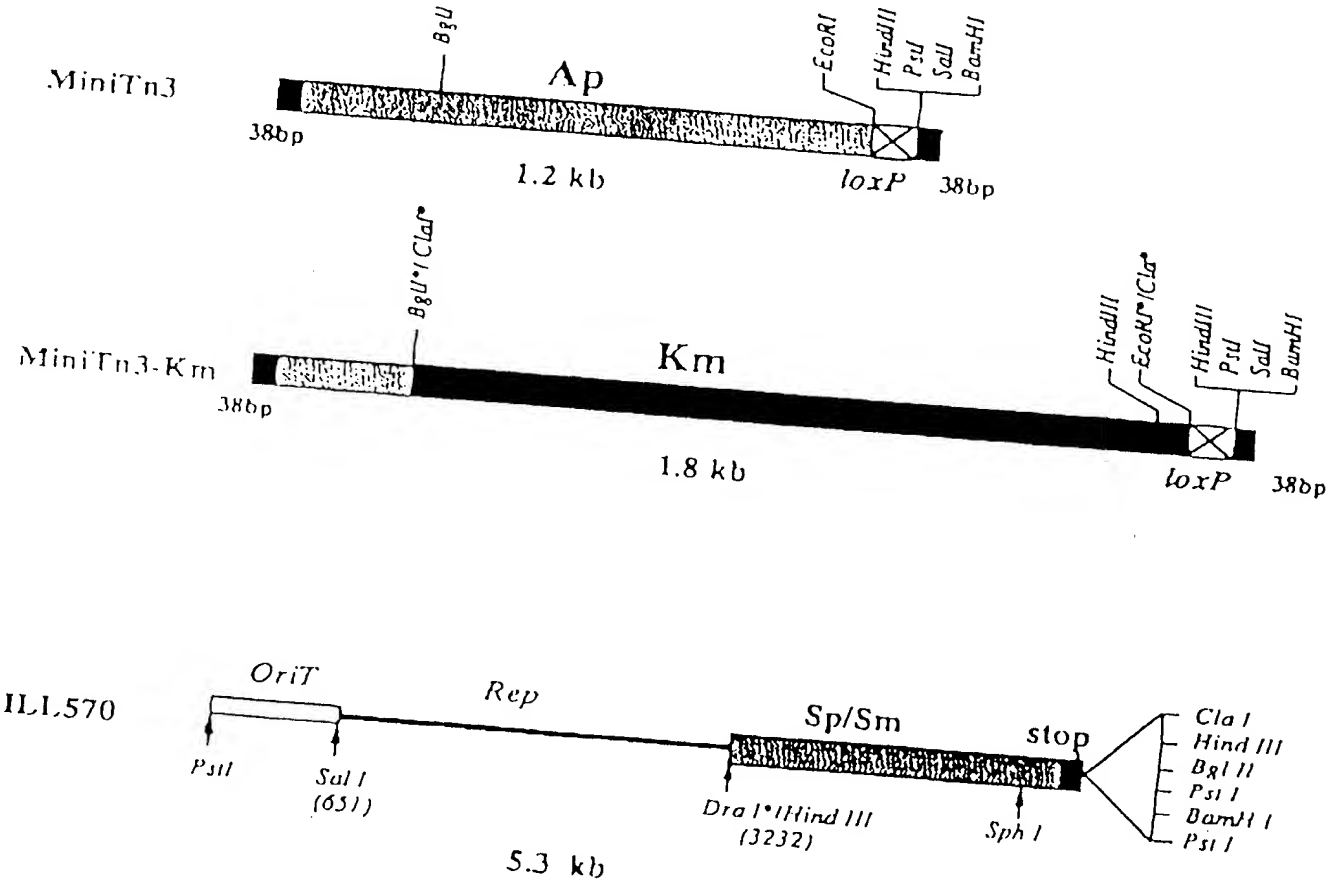
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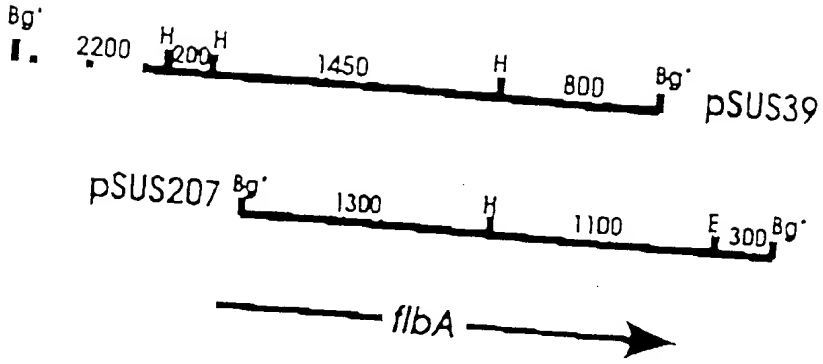
EcoRI
HindIII
PstI
SalI
BamHI
38bp
1.2 kb
loxP
38bp
MiniTn3-Km
Km
BglII*ClaI*
HindIII
EcoRI*ClaI*
HindIII
PstI
SalI
BamHI
38bp
1.8 kb
loxP
38bp
pILL570
OriT
Rep
Sp/Sm
stop
PstI
SalI
(651)
DraI*HindIII
(3232)
SphI
ClaI
HindIII
BglII
PstI
BamHI
PstI
5.3 kb

FIGURE 1A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H
200
H
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H
800
Bg
pSUS39
pSUS207
Bg
1300
H
1100
E
300
Bg
flbA

FIGURE 1B

```
1                                                                  31
AGC TTT TTT GTG CCA TAC TTT TAA ACT TTA TAT TAT AAT AAG AGA CAA ACA CAC CTA CCA

61                                                                 91
AAA TTA AGG CAT TGA TTT TAG ATT ATG GCA AAC GAA CGC TCC AAA TTA GCT TTT AAA AAG
                                M   A   N   E   R   S   K   L   A   F   K   K
121                                                               151
ACT TTC CCT GTC TTT AAA CGC TTC TTG CAA TCC AAA GAC TTA GCC CTT GTG GTC TTT GTG
T   F   P   V   F   K   R   F   L   Q   S   K   D   L   A   L   V   V   F   V
181                                                               211
ATA GCG ATT TTA GCG ATC ATT ATC GTG CCG TTA CCG CCT TTT GTG TTG GAT TTT TTA CTC
I   A   I   L   A   I   I   I   V   P   L   P   P   F   V   L   D   F   L   L
241                                                               271
ACG ATT TCT ATC GCG CTA TCG GTG TTG ATT ATT TTA ATC GGG CTT TAT ATT GAC AAA CCG
T   I   S   I   A   L   S   V   L   I   I   L   I   G   L   Y   I   D   K   P
301                                                               331
ACT GAT TTT AGC GCT TTC CCC ACT TTA TTA CTC ATT GTA ACC TTA TAC CGC TTG GCT TTA
T   D   F   S   A   F   P   T   L   L   L   I   V   T   L   Y   R   L   A   L
361                                                               391
AAT GTC GCC ACC ACT AGA ATG ATT TTA ACC CAA GGC TAT AAA GGG CCT AGC GCG GTG AGC
N   V   A   T   T   R   M   I   L   T   Q   G   Y   K   G   P   S   A   V   S
421                                                               451
ATT ATT ATC ACG GCG TTT GGG GAA TTT AGC GTG AGC GGG AAT TAT GTG ATT GGG GCT ATT
I   I   I   T   A   F   G   E   F   S   V   S   G   N   Y   V   I   G   A   I
481                                                               511
ATC TTT AGT ATT TTA GTG CTG GTG AAT TTA TTA GTG GTT ACT AAT GGT TCT ACT AGG GTT
I   F   S   I   L   V   L   V   N   L   L   V   V   T   N   G   S   T   R   V
541                                                               571
ACT GAA GTT AGG GCG CGA TTT GCC CTA GAC GCT ATG CCA GGA AAG CAA ATG GCG ATT GAT
T   E   V   R   A   R   F   A   L   D   A   M   P   G   K   Q   M   A   I   D
601                                                               631
GCG GAT TTA AAT TCA GGG CTT ATT GAT GAT AAG GAA GCT AAA AAA CGG CGC GCC GCT CTA
A   D   L   N   S   G   L   I   D   D   K   E   A   K   K   R   R   A   A   L
661                                                               691
AGC CAA GAA GCG GAT TTT TAT GGT GCG ATG GAT GGC GCG TCT AAA TTT GTC AAA GGC GAT
S   Q   E   A   D   F   Y   G   A   M   D   G   A   S   K   F   V   K   G   D
721                                                               751
GCG ATC GCT TCT ATC ATT ATC ACG CTT ATC AAT ATC ATT GGG GGT TTT TTA GTG GGC GTG
A   I   A   S   I   I   I   T   L   I   N   I   I   G   G   F   L   V   G   V
781                                                               811
TTC CAA AGG GAT ATG AGC TTG AGC TTT AGT GCT AGC ACT TTC ACT ATC TTA ACC ATT GGC
F   Q   R   D   M   S   L   S   F   S   A   S   T   F   T   I   L   T   I   G
841                                                               871
GAT GGG CTT GTA GGG CAA ATC CCT GCC TTA ATC ATT GCG ACA CGG ACC GGT ATT GTC GCC
D   G   L   V   G   Q   I   P   A   L   I   I   A   T   R   T   G   I   V   A
901                                                               931
ACT CGC ACC ACG CAA AAC GAA GAA GAG GAC TTT GCT TCT AAG CTC ATC ACA CAG CTC ACC
T   R   T   T   Q   N   E   E   E   D   F   A   S   K   L   I   T   Q   L   T
961                                                               991
AAT AAA AGC AAA ACT TTA GTG ATT GTG GGG GCG ATT TAT TGC TTT TGC ACC ATT CCT GGA
N   K   S   K   T   L   V   I   V   G   A   I   Y   C   F   C   T   I   P   G
1021                                                              1051
CTC CCT ACC TTT TCT TTA GCG TTT GTA GGG GCT CTC TTT TTA TTC ATC GCA TGG CTG ATT
L   P   T   F   S   L   A   F   V   G   A   L   F   L   F   I   A   W   L   I
1081                                                              1111
AGC AGG GAG GGA AAG GAC GGG TTG CTC ACT AAA TTA GAA AAT TAT TTG AGT CAA AAA TTC
S   R   E   G   K   D   G   L   L   T   K   L   E   N   Y   L   S   Q   K   F
1141                                                              1171
GGC TTG GAT TTG AGC GAA AAA CCC CAC AGC TCC AAA ATC AAA CCC CAC GCC CCC ACC ACA
G   L   D   L   S   E   K   P   H   S   S   K   I   K   P   H   A   P   T   T
1201                                                              1231
AGG GCT AAA ACC CAA GAA GAG ATT AAA AGA GAA GAA GAG CAA GCC ATT GAT GAA GTG TTA
R   A   K   T   Q   E   E   I   K   R   E   E   E   Q   A   I   D   E   V   L
```

FIGURE 2A

```
1261                                                                1291
AAA ATT GAA TTT TTA GAA TTG GCT TTA GGC TAT CAG CTC TAC AGC TTA GCG GAC ATG AAA
K   I   E   F   L   E   L   A   L   G   Y   Q   L   Y   S   L   A   D   M   K
1321                                                                1351
CAA GGG GGC GAT TTG TTA GAA AGG ATT AGG GGT ATT AGA AAA AAG ATA GCG AGC GAT TAT
Q   G   G   D   L   L   E   R   I   R   G   I   R   K   K   I   A   S   D   Y
1381                                                                1411
GGT TTT TTG ATG CCT CAA ATT AGG ATT AGG GAT AAT TTA CAA CTC CCC CCA ACG CAT TAT
G   F   L   M   P   Q   I   R   I   R   D   N   L   Q   L   P   P   T   H   Y
1441                                                                1471
GAA ATC AAG CTT AAG GGC ATT GTG ATT GGT GAA GGC ATG GTG ATG CCG GAT AAG TTT TTA
E   I   K   L   K   G   I   V   I   G   E   G   M   V   M   P   D   K   F   L
1501                                                                1531
GCC ATG AAT ACC GGT TTT GTG AAT AAA GAA ATT GAA GGC ATT CCT ACT AAA GAG CCG GCT
A   M   N   T   G   F   V   N   K   E   I   E   G   I   P   T   K   E   P   A
1561                                                                1591
TTT GGA ATG GAC GCT TTA TGG ATT GAA ACT AAA AAT AAA GAA GAA GCC ATC ATT CAA GGC
F   G   M   D   A   L   W   I   E   T   K   N   K   E   E   A   I   I   Q   G
1621                                                                1651
TAT ACC ATT ATT GAT CCA AGC ACC GTT ATT GCG ACG CAC ACC AGC GAA TTA GTG AAA AAA
Y   T   I   I   D   P   S   T   V   I   A   T   H   T   S   E   L   V   K   K
1681                                                                1711
TAC GCT GAA GAT TTT ATC ACT AAA GAT GAA GTG AAA TCC CTT TTA GAG CGC TTG GCC AAA
Y   A   E   D   F   I   T   K   D   E   V   K   S   L   L   E   R   L   A   K
1741/591                                                            1771
GAC TAT CCT ACG ATT GTA GAA GAG AGT AAA AAA ATC CCC ACC GGT GCG ATC CGA TCA GTC
D   Y   P   T   I   V   E   E   S   K   K   I   P   T   G   A   I   R   S   V
1801                                                                1831
TTG CAA GCC TTG TTG CAT GAA AAA ATC CCC ATT AAA GAC ATG CTC ACT ATT TTA GAA ACG
L   Q   A   L   L   H   E   K   I   P   I   K   D   M   L   T   I   L   E   T
1861                                                                1891
ATT ACC GAT ATT GCG CCA TTA GTT CAA AAC GAT GTG AAT ATC TTA ACC GAA CAA GTG AGG
I   T   D   I   A   P   L   V   Q   N   D   V   N   I   L   T   E   Q   V   R
1921                                                                1951
GCG AGG CTT TCT AGG GTG ATC ACT AAC GCT TTT AAA TCT GAA GAC GGG CGT TTG AAA TTT
A   R   L   S   R   V   I   T   N   A   F   K   S   E   D   G   R   L   K   F
1981                                                                2011
TTA ACC TTT TCT ACC GAT AGC GAA CAA TTT TTG CTT AAT AAA TTG CGA GAA AAT GGC ACT
L   T   F   S   T   D   S   E   Q   F   L   L   N   K   L   R   E   N   G   T
2041                                                                2071
TCT AAG AGC CTA CTA CTC AAT GTG GGC GAA TTG CAA AAA CTC ATT GAA GCG GTC TCT GAA
S   K   S   L   L   L   N   V   G   E   L   Q   K   L   I   E   A   V   S   E
2101                                                                2131
GAG GCC ATG AAA GTC TTG CAA AAA GGG ATC CCT CCG GTG ATT TTG ATC GTA GAG CCT AAT
E   A   M   K   V   L   Q   K   G   I   A   P   V   I   L   I   V   E   P   N
2161                                                                2191
TTA AGA AAA GCC CTT TCT AAT CAA ATG GAG CAG GCT AGG ATT GAT GTA ATC GTG CTA AGC
L   R   K   A   L   S   N   Q   M   E   Q   A   R   I   D   V   I   V   L   S
2221                                                                2251
CAT GCT GAA TTA GAT CCT AAC TCT AAT TTT GAA GCC TTA GGC ACG ATC CAT ATT AAC TTT
H   A   E   L   D   P   N   S   N   F   E   A   L   G   T   I   H   I   N   F
2281                                                                2311
TAA GGG ATA AAT AAT TGA TAA AAA AGG AGA ATG ATG CAA GTT TAT CAC CTT TCA CAC ATT
*
2341                                                                2371
GAT TTA GAC GGC TAT GCA TGC CAG CTT GTT TCA AAA CAA TTT TTT AAA AAT ATC CAA TGC
2401                                                                2431
TAT AAC GCT AAT TAC GGG CGT GAA GTC TCA GCC AGA ATT TAT GAG ATT TTA AAC GCG ATC
2461                                                                2491
GCT CAA TCT AAA GAG AGT GAA TTC CTT ATT TTG ATT AGC GA
```

FIGURE 2B

```
  1 MANERS-KLAFKKTFPVFKRFLQSKDLALVVFVIAILAIIIVPLPPFVLDFLLTISIALS HpFlbA
  1 MAQNKIVDLVFPFLGPLIAPVLKAKSLTIVGFLVCILAIIIVPLPSPILDFFLALSIALS CjFlbA
  1 MADAAAPNASSMPSAKSLLDGLMRGEMGLALGVVGIIVLLIIPVPAPLLDVLLAISLTGS CcFlbF
  1 ---------MNPHDLEWLNRIGERKDIMLAVLGLAVVFMMVLPLPPLVLDILIAVNMTIS YpLcrD
  1 ------ ------MLLSLLNSARLRPRLGILVLMVMIISMFVIPLPTYLVDFLIALNIVLA StInvA
  1 ------------------------------MVMIIAMLIIPLPTYLVDFLIGLNIVLA SfMxiA

 60 VLIILIGLYIDKPTDFSAFPTLLLIVTLYRLALNVATTRMILTQGYKGPSAVSIIITAFG HpFlbA
 61 VLIIGISIYIPKPTDLTTFPTLILIITLFRLSLNIATTRMILSEGQNGPEAVSEIIAAFG CjFlbA
 61 VLILMTAIGIKKPLEFTSFPTVLLVTTLFRIGLNIASTRLILSHGQEGTGGAGAVIEAFG CcFlbF
 52 VVLLMIAIYINSPLQFSAFPAVLLVTTLFRLALSVSTTRMILLQ-----ADAGQIVYTFG YpLcrD
 49 ILVFMGSFYIDRILSFSTFPAVLLITTLFRLALSISTSRLILIEA-----DAGEIIATFG StInvA
 29 ILVFMGSFYIERILSFSTFPSVLLITTLFRLALSISTSRLILVDADRGK-----IITTFG SfMxiA

120 EFSVSGNYVIGAIIFSILVLVNLLVVTNGSTRVTEVRARFALDAMPGKQMAIDADLNSGL HpFlbA
121 EFVVGGNMVIGVIVFCILVLINFMVVTKGSTRVSEVQARFTLDAMPGKQMAIDADLNAGL CjFlbA
121 HLMMQGNFVIGVIVFIILIVVNFMVVTKGSGRIAEVAARFTLDSMPGKQMAIDADLSTGL CcFlbF
107 NFVVGGNLIVGIVIFLIITIVQFLVITKGSERVAEVSARFSLDAMPGKQMSIDGDMRAGV YpLcrD
104 QFVIGDSLAVGFVVFSIVTVVQFIVITKGSERVAEVAARFSLDGMPGKQMSIDADLKAGI StInvA
 84 QFVIGDSLAVGFVIFSIVTVVQFIVITKGSERVAEVAARFSLDGMPGKQMSIDADLKAGI SfMxiA

180 IDDKEAVGRRAALSQEADFYGAMDGASKFVKGDAIASIIITLINIIGGFLVGVFQRDMSL HpFlbA
181 IDEQTARARRQEVIAEANFYGAMDGSSKFIKGDAVAGIIITIINIIGGFLIGSFQHDMAL CjFlbA
181 ISQDEAKIRRKELEQESTFFGAMDGASKFVKGDAIAGLIITAINIIGGIIIGVVQHKMPF CcFlbF
167 IDVNEARERRATIEKESQMFGSMDGAMKFVKGDAIAGLIIIFVNILGGVTIGVTQKGLAA YpLcrD
164 IDADAARERRSVLERESQLYGSFDGAMKFIKGDAIAGIIIIFVNFIGGISVGMTRHGMDL StInvA
144 IDAAGAKERRSILERESQLYGSFDGAMKFIKGDAIAGIIIIFVNLIGGISVGMSQHGMSL SfMxiA

240 SFSASTFTILTIGDGLVGQIPALIIATRTGIVATRTTQNEEEDFASKLITQLTNKSKTLV HpFlbA
241 SDAASTYTILTIGDGLVSQIPGLITSTATAIIITRASKDEENFAEGTLTQLLSEYRTLLI CjFlbA
241 GDAASTYTIMTIGDGLVSQIPALIISIAAGMVVSKAGVEGSADKALTTQLAMQPVGLGMV CcFlbF
227 AEALQLYSILTVGDGMVSQVPALLIAITAGIIVTRVSSEDSSDLGSDIGKQVVAQPKAML YpLcrD
224 SSALSTYTMLTIGDGLVAQIPALLIAISAGFIVTRVNGDTDN-MGRNIMTQLLNNPFVLV StInvA
204 SGALSTYTILTIGDGLVSQIPALLISISAGFMLTRVNGDSDN-MGRNIMSQIFGNPFVLI SfMxiA

300 IVGAIYC-FCTIPGLPTFSLAFVGALFLFIAWLISREGKDGLLTKLENYLSQKFGLDLSE HpFlbA
301 VGFVLFI-FALVPGLPTLSLGFMALVFLSLGYLTKQVKEGKI-----DITTVKKSKPSAA CjFlbA
301 SASSG-I-IALIPGMPIFPFAAMALA----------AGALAY CcFlbF
287 IGGVLLLLFGLIPGFPTVTFLILALLVGCGGYMLSRKQSRNDFANQDLQSILTSGSGAPA YpLcrD
283 VTAILTISMGTLPGFPLPVFVILSVVLSVLFYFKFREAKRSAAKPKTSKGEQPLSIEEKE StInvA
263 VTSALALAIGMLPGFPFFVFFLIAVTLTALFYYKKVVEKEKSLSESDSSGYTG------- SfMxiA

359 KPHSSKIKPHAPTTRAKTQEEIKREEEQAIDEVLKIEFLELALGYQLYSLADMKQGGDLL HpFlbA
355 VASQSGAGGTTAAPAKKSEEEILKEEEHKINDILKVEILELELGYGLIKLAE----NELT CjFlbA
331 KRVQDAKKPKALDPADLEAAAPSEPEEEPISASLAIDDVKIELGYGLLTLINDLDGRKLT CcFlbF
347 ARTKAKTSGANKGRLGEQEAFAMTVPLLIDVDS----------SQQEALEANALN YpLcrD
343 GSSLGLIGDLDKVSTE----------TVPLILLVPKSRREDLEKA StInvA
316 ----------TFDIDNTHDSSLAMIENLDRISSETVPLILLFAENKINANDME SfMxiA
```

FIGURE 3A

```
419 ERIRGIRKKIASDYGFLMPQIRIRDNLQLPPTHYEIKLKGIVIGRGMVMPDKFLAMNTGF HpF1bA
411 ERIRSMRRSIAESLGFLMPKIRIRDNLRLKPNEYSFKLKGVSIASAEIYPDKYLAMDSGF CjF1bA
391 DQIRALRKTLASEYGFVMPPVRILDNMRLANQGYAIRIKEMEAGAGEVRLGCLMCMDPRG CcF1bF
392 DELVRVRRALYLDLGVPFPGIHLRFNEGMGEGEYIISLQEVPVARGELKAGYLLVRESVS YpLcrD
378 QLAERLRSQFFIDYGVRLPEVLLRDGRGLDDNSIVLLINEIRVEQFTVYFD--LMRVVNY StInvA
359 GLIERIRSQFFIDYGVRLPTILYRTSNELKVDDIVLLINEVRADSFNIYFDKVCITDENG SfMxiA

479 VNKEIEGIPTKEPAF--GMDALWIETQNKEEAIIQGYTIIDPSTVIATHTSELVKKYAED HpF1bA
471 ITEEIEGIATKEPAF--NSDALWIDANLKDEATLNGYIVIDPASVISTHMSELIKAHASE CjF1bA
451 GQVELPGEHVREPAF--GLPATWIADDLREEATFRGYTVVDPATVLTTHLTEILKENMAD CcF1bF
452 QLELLGIPYEKGEHLLPDQEAFWVSVEYEERLEKSQLEFFSHSQVLTWHLSHVLREYAED YpLcrD
436 SDEVVSFGINPTIHQQGSSQYFWVTHEEGEKLREIGYVLRNALDELYHCLAVTVARNVNE StInvA
419 DIDALGIPVVSTS--YNERVISWVDVSYTENLTNIDAKIKSAQDEFYHQLSQALLNNINE SfMxiA

537 FITKDEVKSLLERLANDYPTIVEESK-KI-PTGAIRSVLQALLHEKIPIKDMLTILETIT HpF1bA
529 LLTRQEVQNLLDKVKNDYPIIVEGAL-GVAPVSLIQKILKDLLKHHIPIKDMLTILESVS CjF1bA
509 LLSYAEVQKLLKELPETQKKLVDDLIPGTVTATTVQRVLQSLLRERVSIRDLPQILEGVG CcF1bF
512 FIGIQETRYLLEQMEGGYGELIKEVQR-IVPLQRMTEILQRLVGEDISIRNMRSILEAMV YpLcrD
496 YFGIQETKNMLDQLEAKFPDLLKEVLRH-ATVQRISEVLQRLLSERVSVRNMKLIMEALA StInvA
477 IFGIQETKNMLDQFENRYPDLLKEVFRHV-TIQRISEVLQRLLGENISVRNLKLIMESLA SfMxiA

595 DIAPLVQNDVNILTEQVRAPLSRVITNAFKSEDGRLKFLTFSTDSEQFLLNKLRENGTSK HpF1bA
588 DIAE-VSKSFDMIIEHVRASLARMITNMYLDDKGNLDIFILDSASSAVLMENVQFRDGSY CjF1bA
569 EAAPHTA-SVTQLVEQVRARLAROLCWANRGDDGALPIITLSADWEQAFAEALIGPGDDK CcF1bF
571 EWGQK-EKDVVQLTEYIRSSLKRYICYKYANGNNILPAYLFDQEVEEKIRSGVRQTSAGS YpLcrD
555 LWAPR-EKDVINLVEHIRGAMARYICHNF-ANGGELPAVMVSAEVEDVIRKGIRQTSGST StInvA
536 LWAPR-EKDVITLVEHVRASLSRYICSK-IAVSGEIKVVMLSGYIEDAIRKGIRQTSGGS SfMxiA

655 SLLLNVGELQKLIFAVSEENMKVLQKGIAPVILIVEPNLRKALSNQMEQARIDVIVLSHA HpF1bA
647 KLPLSVAQTGTLVDTLRAEVAAVANGRIKPFILCVEPQLRKFIADICYNFSINIVVLSFA CjF1bA
628 QLALPPSRLQDFIRGVRDSFERAALAGEAPVLL-TSPGVRPYVRSIIERFRGQTVVMSQN CcF1bF
630 YLALEPAVTESLLEQVRKTIGDLSQIQSKP-VLIVSMDIRRYVRKLIESEYYGLPVLSYQ YpLcrD
613 FLSLDPEASANLMDLITLKLDDLLIAH-KDLVLLTSVDVRRFIKKMIEGRFPDLEVLSFG StInvA
594 FLNMDIEVSDEVMETLAHALREL-RNAKQNFVLLVSVDIRRFVKRLIDNRFKSILVISYA SfMxiA

715 ELDPNSNFEALGTIHINF                                    HpF1bA
707 EIAENINFNTEGIIRIEL                                    CjF1bA
687 EIMPRARLKTVGMV----                                    CcF1bF
689 ELTQQINIQPLGRICL--                                    YpLcrD
672 EIADSKSVNVIKTI----                                    StInvA
653 EIDEAYTINVLKTI----                                    SfMxiA
```

FIGURE 3B

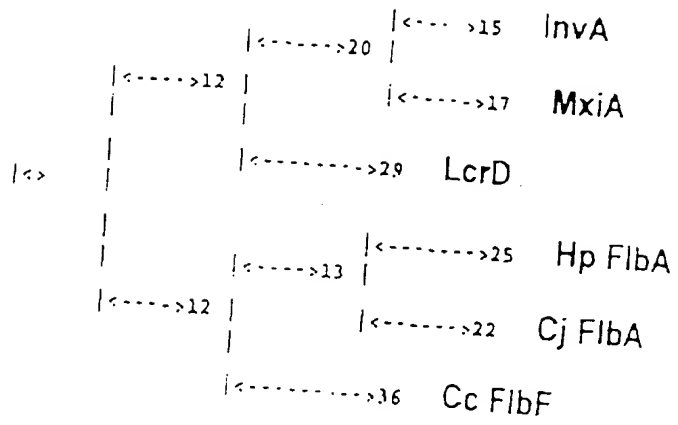


FIGURE 4

1) PCR amplification

2) Cloning the PCR product in pSUS33

3) Insertion of the Km cartridge

4) Electroporation in H. pylori N6

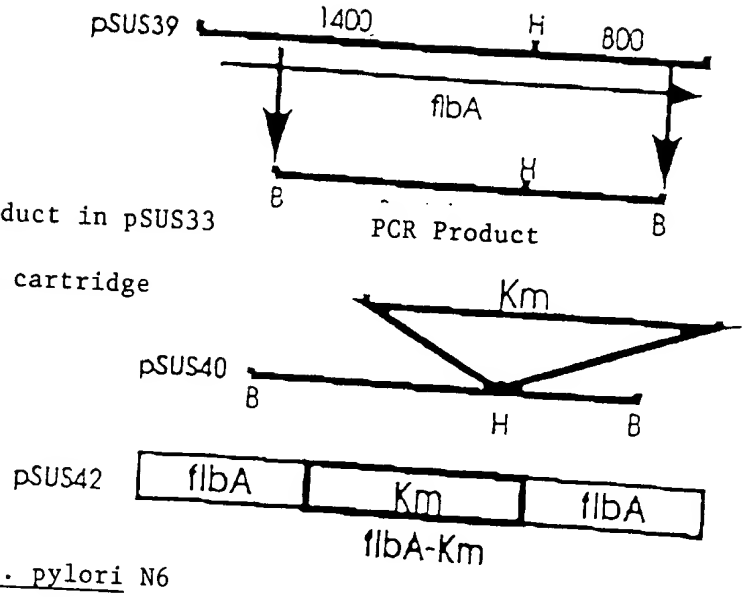


FIGURE 5

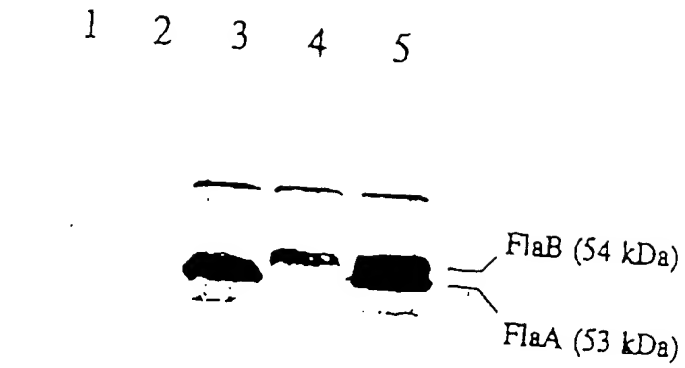


FIGURE 6

Distribution of the 300 FNTS serums relative
to the unscouraged N6f1BA strain
Extraction by means of N-octyl-glucoside

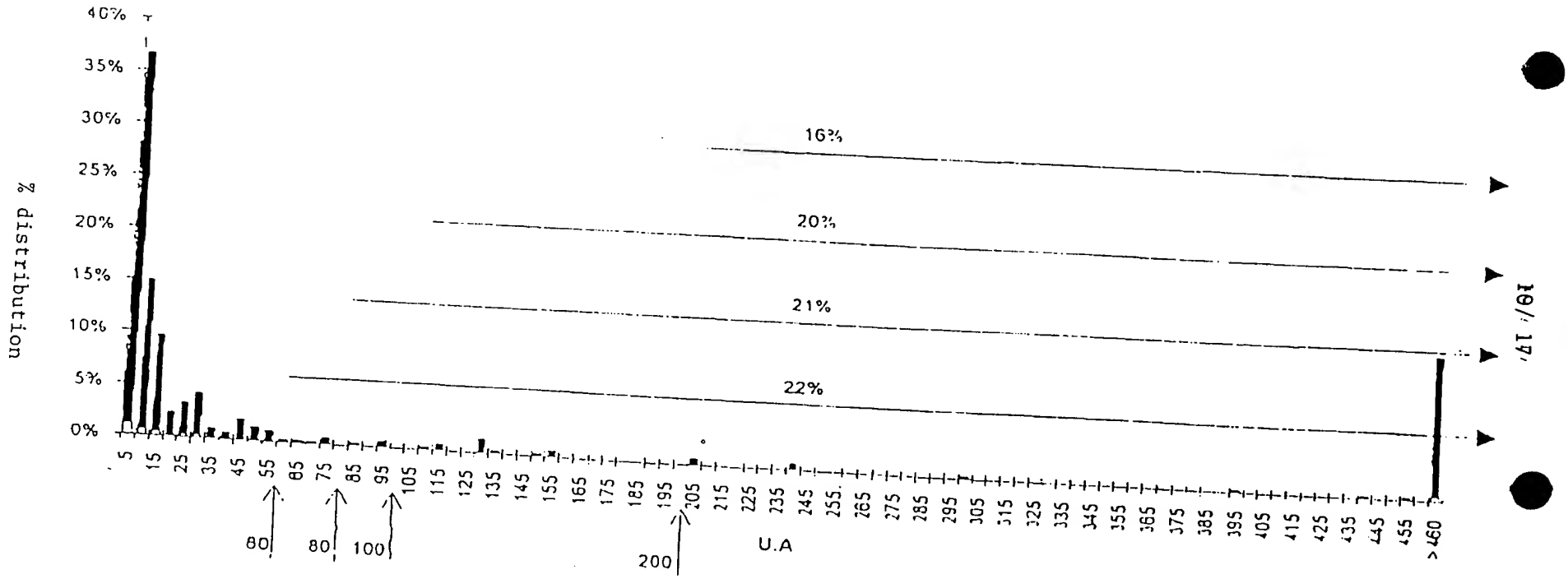


FIGURE 7

Distribution of the 300 FNTS serums relative to the scourged N6 strain
Extraction by means of N-octyl-glucoside

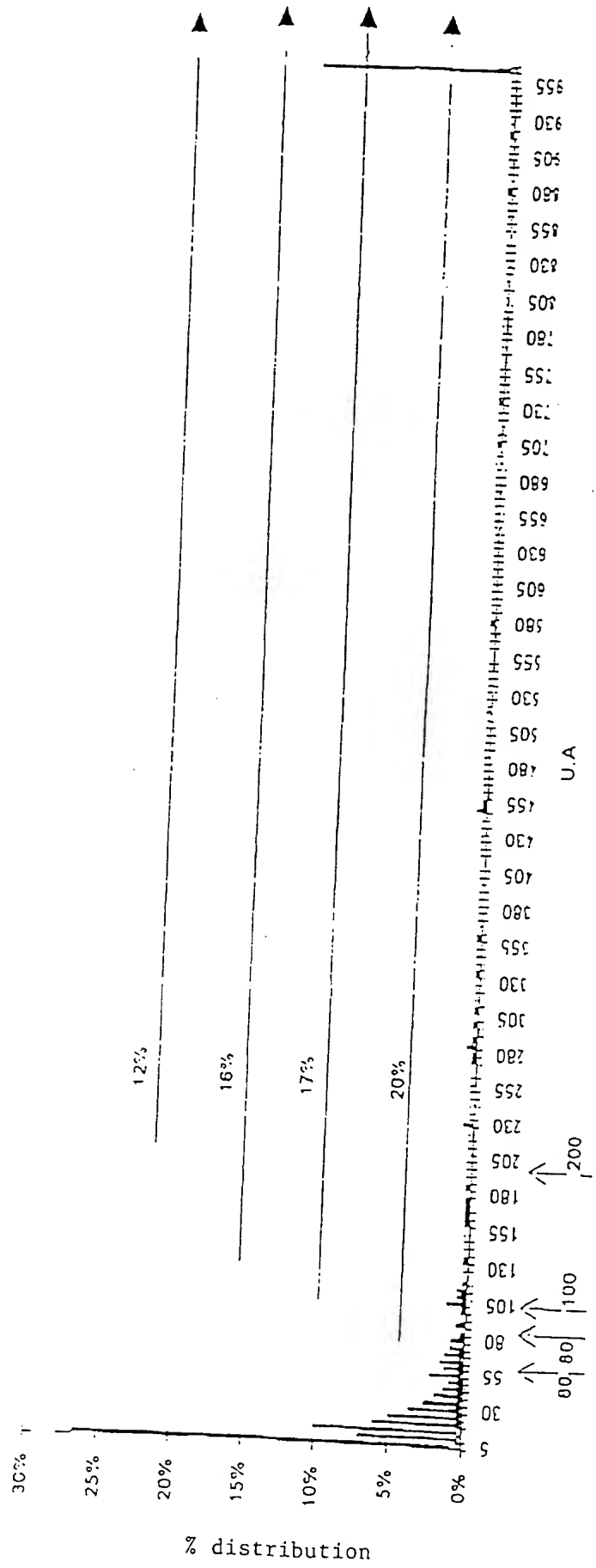


FIGURE 8

Distribution of the 300 FNTS serums relative to the
unscouraged N6f1BA strain --
Extraction by means of PBS

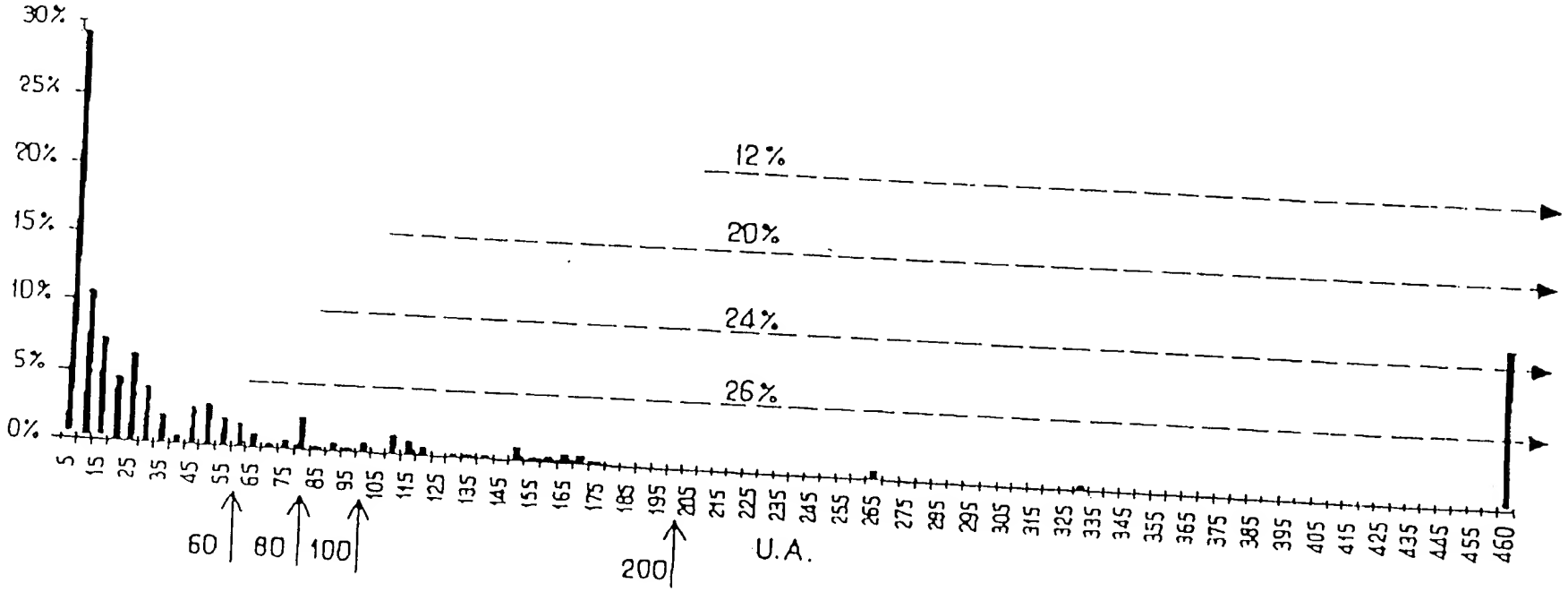


FIGURE 9

The presence of positiveness in 43 FNTS serums

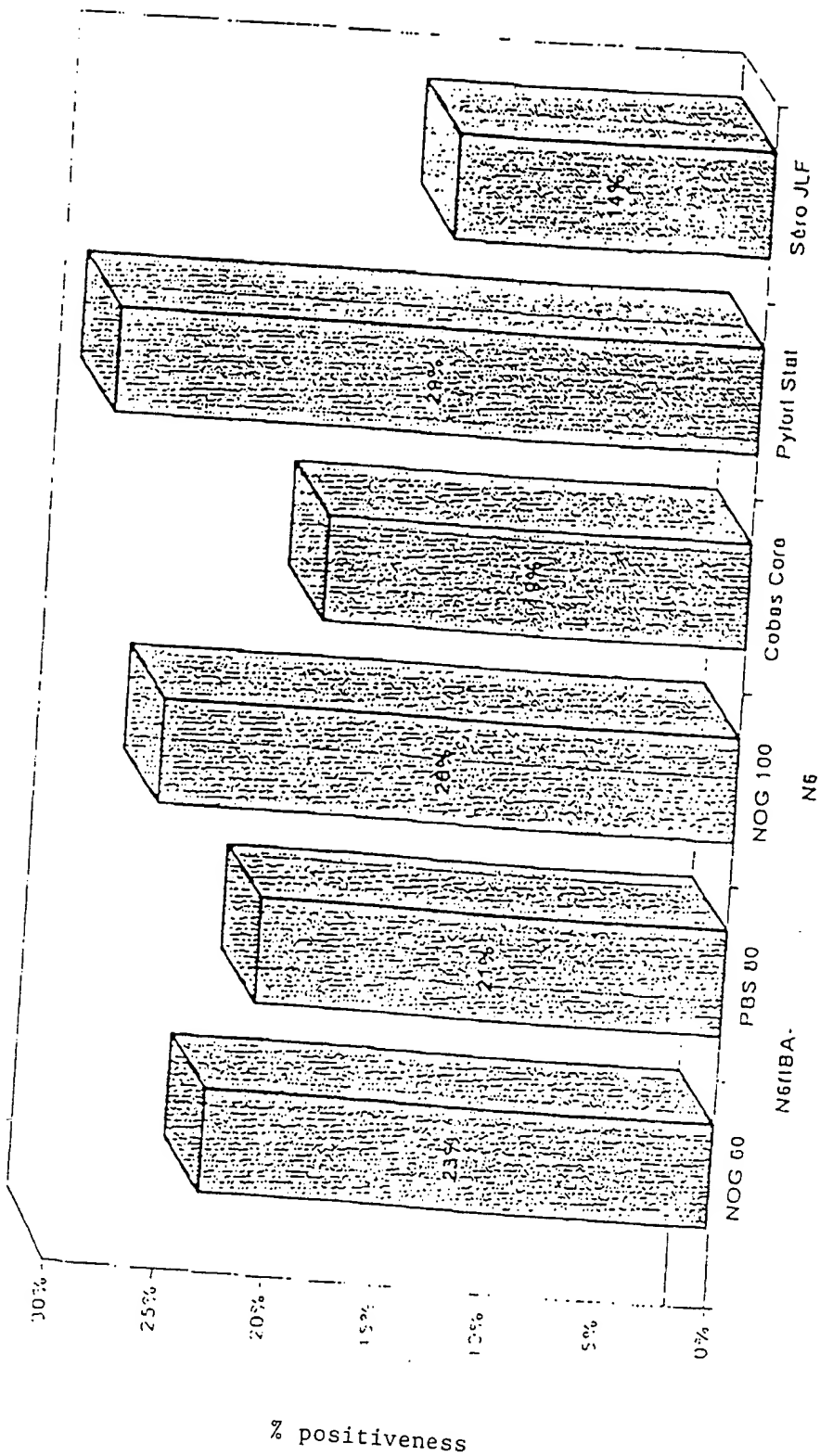


FIGURE 10

The ROC curve of the N6f1BA N-octyl-glucoside extract

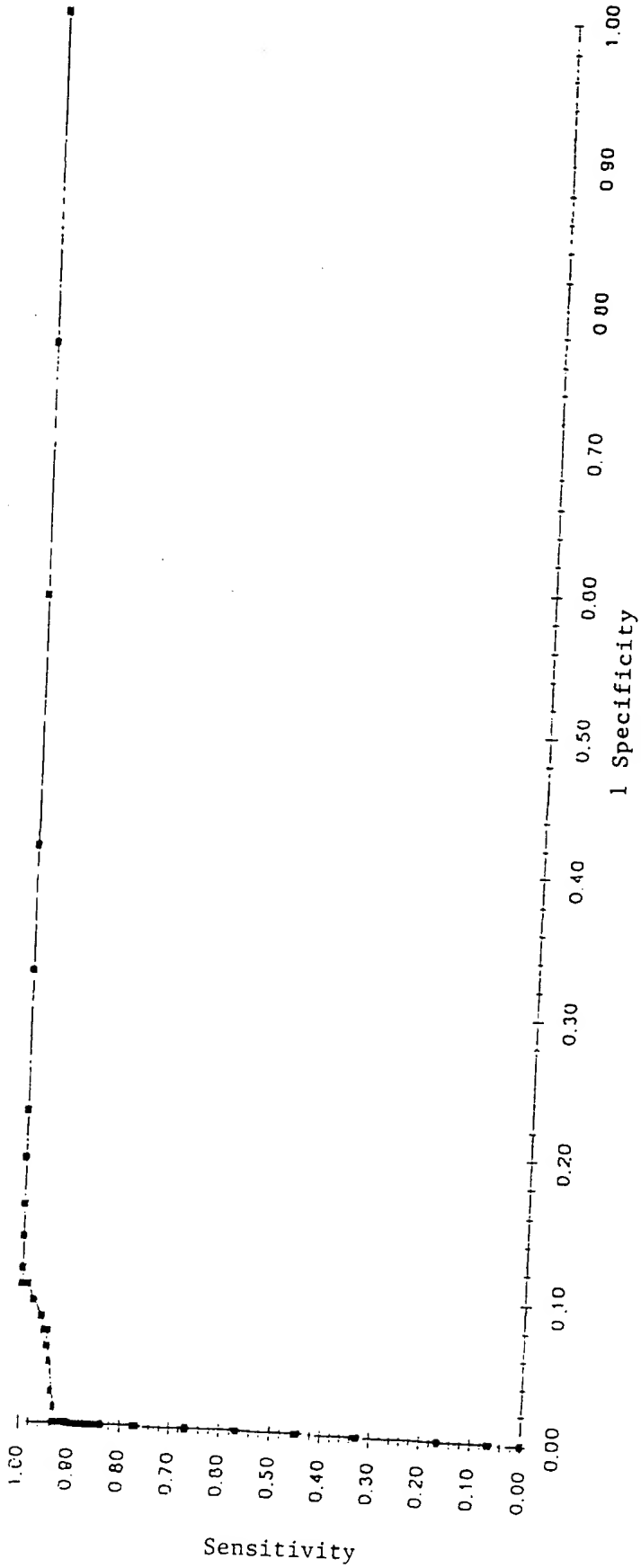
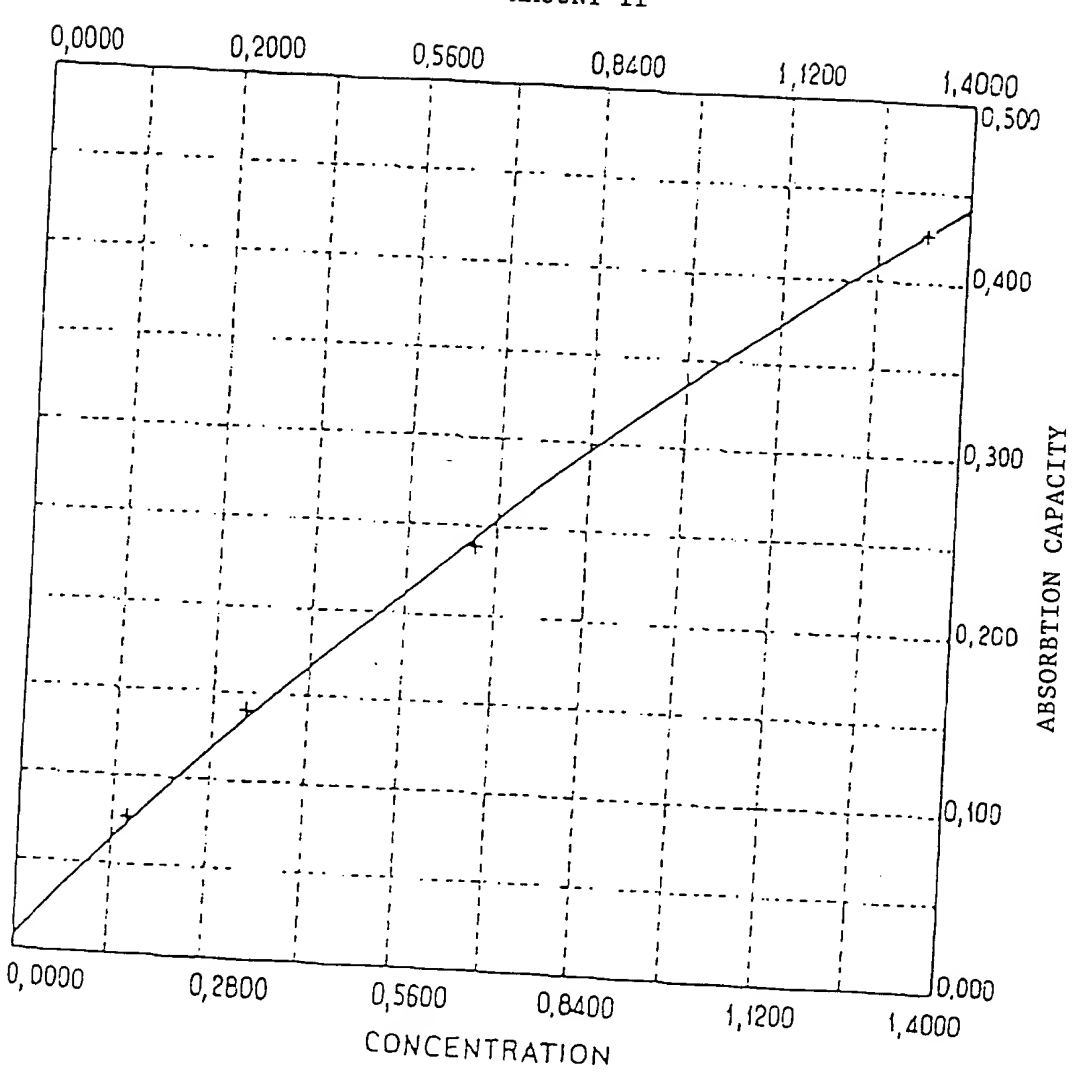


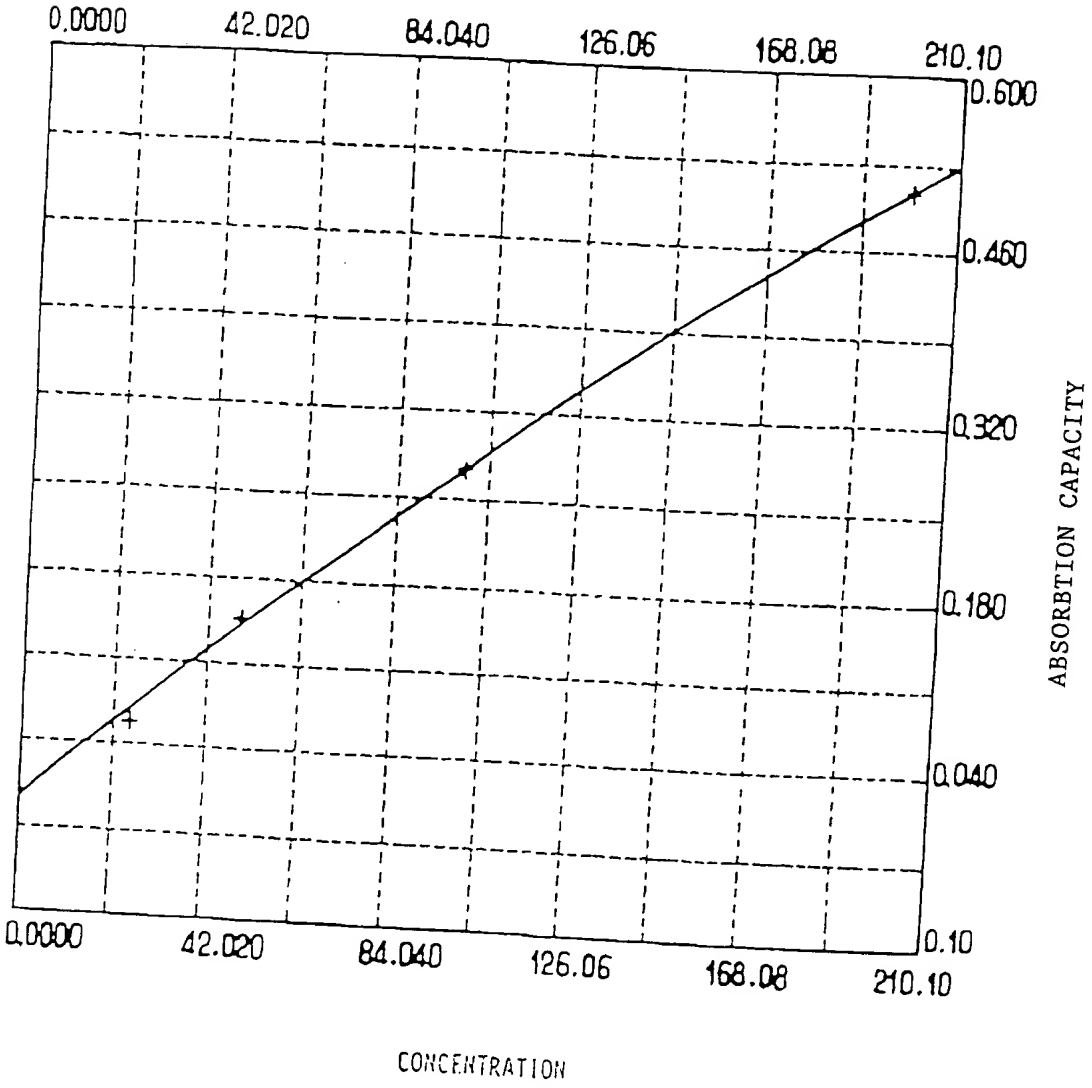
FIGURE 11

FIG_12



Type of extract	DO @750nm	concentration in mg/ml
Glycine (after centrifugation for 15 min @ 3000 g)	0,028	0,284
N-octyl-glycoside	0,087	1,004
Supernatant 1 (after 1st PBS washing)	0,059	0,844
Supernatant 2 (after 2nd PBS washing)	0,015	0,1105

FIG_13(A)


0.0000
42.020
84.040
126.06
168.08
210.10
0.600
0.460
0.320
0.180
0.040
0.10
ABSORBTION CAPACITY
CONCENTRATION

Type of extract	DO @ 760 nm	concentration in µg/ml
Glycine (after centrifugation for 15 min @ 3000g)	0.279	202.86
N-octyl-glucoside	0.243	873.99
Supernatant 1 (after 1st PBS washing)	0.361	539.2
Supernatant 2 (after 2nd PBS washing)	0 218	77.875

Type of extract	DO @ 760 nm	concentration in µg/ml
Glycine residue (after 15 min of centrifugation at 3000g)	0.099	297.5
Glycine residue (after extraction)	0.093	2778.7
N-octyl-glucoside (after extraction)	0 275	972.0

FIGURE 13B